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hERG CHANNEL-EXPRESSING CELL

CROSS REFERENCE TO PRIOR RELATED APPLICATIONS

This application is a U.S. national phase application under 35 U.S.C. § 371 of International Patent Application No. PCT/JP2004/017441, filed November 17, 2004 and claims the benefit of Japanese Patent Application No. 2003-387255, filed November 17, 2003, both of which are incorporated by reference herein. The International Application was published in Japanese on May 26, 2005 as International Publication No. WO 2005/047500 A1 under PCT Article 21(2).

TECHNICAL FIELD

The present invention relates to cells for evaluation in order to avoid the risk of adverse effects on the heart caused by electrocardiographic QT interval prolongation which is a big safety problem in research and development of drugs, as well as methods for establishing such cells and evaluation of drugs using the established cells.

BACKGROUND ART

Safety pharmacological studies are non-clinical studies to examine the safety of novel drugs on human from pharmacological viewpoints. Guideline on Safety Pharmacology Studies which aims at examining the safety of test substances on human and predicting adverse effects thereof has been set in the International Conference on Harmonisation of Technical Requirements for Registration of Pharmaceuticals for Human Use (ICH) between Europe, Japan and the United States. According to the Guideline, examination of the arrhythmogenic effect, in particular, the presence or absence of electrocardiographic QT interval prolongation effect, of test substances is required as a part of safety pharmacological studies. In order to protect patients from ventricular tachycardia, torsades de pointes and lethal arrhythmia associated with QT interval prolongation induced by drug administration, it is very important in the development of drugs to detect QT interval prolongation effect which may induce such serious adverse effects.

To date, it has been known that a large number of drugs having QT interval prolongation effect inhibit delayed rectifier potassium channels in cardiomyocytes. It is believed that hERG (human ether-a-go-go related gene) channel is functioning as a major constituent protein in the delayed rectifier potassium channel. Therefore, in the draft

guideline for non-clinical evaluation of the potential for delayed ventricular repolarization (QT Interval Prolongation) by human pharmaceuticals (ICH-S7B), ion channel assay using hERG channel-transferred cells is recommended as a non-clinical study.

Conventionally, as a method of appropriately evaluating the effect of a compound on hERG channels, the patch clamp technique has been used in which channel activities of cells that had been allowed to express hERG channels or cardiomyocytes inherently possessing hERG channels are recorded by direct use of glass microelectrodes to the cells or cardiomyocytes (Neher, E. and Sakmann, B., Nature, Vol 260, 779-802, (1976)). However, though this patch clamp technique enables appropriate evaluation of drugs on hERG channels with high accuracy, it has the following problems. That is, it requires highly skilled technology, has a remarkably low throughput (1-5 compounds/day/person) and thus is remarkably insufficient in throughput for a great number of candidate compounds at the development stage of drugs.

On the other hand, as methods for enhancing the throughput of hERG channel evaluation, a method of detecting the release of a radioactive isotope Rb^{3+} (Cheng, C.S. et al., Drug Dev. Ind. Pharm. vol. 28, 177-191, (2002)), a method in which competitive binding to a radioactive isotope tritium (^3H)-labeled dofetilide is observed and evaluated (Finlayson, K. et al. Eur. J. Pharm. vol. 430, 147-148 (2001)) and a method using membrane potential sensitive dyes (Tang, W. et al. J. Biomol. Screen vol. 6, 325-331 (2001); Baxter, D. F. et al. ibid. vol. 7, 79-85 (2003)) have been reported. However, these methods are complicated in operations because radioactive substances are used. Besides, since they are indirect methods, their sensitivity and accuracy are low and far from the measurement accuracy that can be obtained by the patch clamp technique.

Recently, fully automated high throughput patch clamp systems which evaluate the influence by hERG channels appropriately and at the same time have a high throughput have been developed as means to solve the above-described problems. Some of such instruments have been commercialized (IonWorks HT™ from Molecular Device; PatchXpress™ 7000A from Axon Instruments). These apparatuses are intended to suspend hERG channel-expressing cells, suck the cells into a small hole located at the center of each well utilizing dropping by gravity and negative pressure, and to thereby make the cells capable of current recording. Therefore, the highly skilled technology required in the patch clamp technique is not necessary. Besides, the throughput of compounds is very high; data from more than 3000 points can be obtained per day. However, for making evaluation with such an apparatus, hERG channel-expressing cells used in experiments are extremely important. While it is possible to select hERG channel high expressing cells for measuring

in the conventional patch clamp technique where a single cell is selected and evaluated, it is impossible to select high expressing cells in measurement with a fully automated high throughput patch clamp system because cells present are used at random. Therefore, in order to evaluate multiple samples accurately with a fully automated high throughput patch clamp system, more than a specific ratio of cells must be expressing hERG channels and yet the expression levels must be sufficient. Various attempts have been made to prepare hERG channel-expressing cells which can be used in this fully automated high throughput patch clamp system.

According to reports so far made, stably expressing cells were obtained by introducing hERG gene into cells by transfection using the calcium phosphate method or lipofection and then performing extremely labor-consuming procedures such as cloning cells by the limiting dilution culture method and confirming the quantity of transferred hERG gene, or measurement of currents through hERG channels (Tang, W. et al. J. Biomol. Screen, vol. 6 325-331 (2001); Assay and Drug Development Technologies, 1(2-3), 127-135, 2003). However, these techniques cannot secure a sufficient quantity of transferred hERG gene even by spending a great labor of cloning by the limiting dilution culture method, which results in a very weak hERG current per cell. When the hERG current is small, it is impossible to obtain a sufficient S/N ratio and, as a result, measurement sensitivity decreases. Further, even when a cell with whatever large hERG current has been obtained by cloning, it is often difficult to measure the amplitude of the hERG current with high sensitivity with a fully automated high throughput patch clamp system.

In measurement of currents in the ion channel into which hERG channel is classified, influence of the ion channel which cells endogenously have varies by cell species. Therefore, the practical value of measurement often varies greatly by changing cell species. For this reason, it was also necessary to repeat labor-consuming operations such as described above when measurement was performed with a different cell species.

DISCLOSURE OF THE INVENTION

The present invention has been made under such circumstances. It is an object of the present invention to establish a method of establishing a cell with a remarkably high hERG channel expression level for use in predicting adverse effects based on hERG channel inhibition in research and development of drugs, and to thereby establish a highly sensitive and high throughput evaluation method for test substances.

As a result of extensive and intensive researches toward the solution of the above-described problems, the present inventors have succeeded in obtaining a hERG

channel high expressing cell by inserting a hERG gene into a retrovirus vector plasmid or lentivirus vector plasmid to thereby prepare a virus vector, concentrating the vector by ultracentrifugation if necessary, and transferring the hERG gene into cells. The inventors have also found that, with the resultant cell, it is possible to secure an expression level effective in measurement using a fully automated high throughput patch clamp system or dyes. Thus, the present invention has been achieved.

The present invention has such aspects as:

A hERG channel-expressing cell population containing cells capable of expressing a channel of which the hERG current as determined by patch clamping with a fully automated high throughput patch clamp system is 0.6 nA or more, wherein the ratio of the cells is 40% or more relative to the total number of hERG gene-transferred cells within the population;

The cell population according to the above aspect, wherein the hERG gene has been transferred with a virus vector;

The cell population according to the above aspect, wherein the virus vector is a retrovirus vector or a lentivirus vector;

The cell population according to any one of the aspects above, wherein the average value of hERG current in the total cells is 0.3 nA or more;

A cell capable of expressing a hERG channel of which the hERG current as determined by patch clamping with a fully automated high throughput patch clamp system is 1.0 nA or more;

The cell according to the above aspect, wherein the hERG gene has been transferred with a virus vector;

The cell according to the above aspect, wherein the virus vector is a retrovirus vector or a lentivirus vector;

A method of preparing the cell population or the cell according to any one of the aspects above, which includes expressing hERG channels using a virus vector;

The method according to the above aspect, wherein the virus vector is a retrovirus vector or a lentivirus vector;

The method according to the above aspect, wherein the virus vector is a retrovirus vector;

The method according to one of the aspects above, which includes a step of concentrating the virus vector by ultracentrifugation;

A method of measuring hERG current inhibitory activity, which includes using the cell population or the cell according to one of the aspects above;

The method according to the above aspect, which includes using a fully automated high throughput patch clamp system;

A method of measuring hERG current inhibitory activity, which includes using a cell population or a cell prepared by the method according to one of the aspects above;

The method according to the above aspect, which includes using a fully automated high throughput patch clamp system;

A method of screening for compounds, or salts thereof, that alter or do not alter hERG currents, which includes using the cell population or the cell according to one of the aspects above;

The method according to the above aspect, which includes using a fully automated high throughput patch clamp system;

A method of screening for compounds, or salts thereof, that alter or do not alter hERG currents, which includes using a cell population or a cell prepared by the method according to one of the aspects above; and

The method according to the above aspect, which includes using a fully automated high throughput patch clamp system.

According to the present invention, a method of establishing a cell with a remarkably high hERG channel expression level for use in predicting adverse effects based on hERG channel inhibition in research and development of drugs has been established; with that method, highly sensitive and high throughput evaluation has become possible.

Further, according to the present invention, hERG channel high expressing cells can be obtained simultaneously and efficiently. With this advantage, by allowing a wide variety of cell species to express hERG channel at high levels and comparing influences of endogenous ion channels among those cell species, it has become possible to select the most suitable cell species for predicting adverse effects in research and development of drugs. Further, the hERG channel-expressing cell or hERG channel-expressing cell population of the present invention is capable of expressing hERG channels stably for a long period of time.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 shows the structure of a retrovirus vector plasmid (pBabeXIP).

Fig. 2 shows the structure of a retrovirus vector plasmid (pBabeXIH).

Fig. 3 shows the structure of a retrovirus vector plasmid (pBabeCLXIP).

Fig. 4 shows the structure of a retrovirus vector plasmid (pBabeCLXIH).

Fig. 5 shows the structure of a retrovirus vector plasmid (pBabeCLXI2G).

Fig. 6 shows the structure of a retrovirus vector plasmid (pBabeCLXaIN).

Fig. 7 shows the structure of a hERG gene-transferred retrovirus vector plasmid

(pBabeCL(hERG)aIN).

Fig. 8 shows the structure of a hERG gene-transferred retrovirus vector plasmid (pBabeCL(hERG)IH).

Fig. 9 shows the structure of a hERG gene-transferred retrovirus vector plasmid (pBabeCL(hERG)IP).

Fig. 10 shows the structure of a hERG gene-transferred retrovirus vector plasmid (pBabeCL(hERG)I2G).

Fig. 11 shows the structure of a hERG gene-transferred retrovirus vector plasmid (pBabeCL(hERG)).

Fig. 12 shows the structure of a lentivirus vector plasmid (pLenti6/MCS).

Fig. 13 shows the structure of a lentivirus vector plasmid (pLenti6/cPPT-XI2G).

Fig. 14 shows the structure of a hERG gene-transferred lentivirus vector plasmid (pLenti6/cPPT-(hERG)I2G).

Fig. 15 shows the results of detection of hERG channel protein by Western blotting. (Lane 1: normal CHO-K1 cells; Lane 2: cell strain into which hERG gene was transferred by lipofection; Lane 3: cell strain into which hERG gene was transferred with retrovirus).

Fig. 16 shows the distribution of hERG currents. (A: cell strain into which hERG gene was transferred by lipofection; B: cell into which hERG gene was transferred with retrovirus; C: cell strain into which hERG gene was transferred with retrovirus).

Fig. 17 shows the distribution of hERG currents analyzed with cut-off values. (A: cell strain into which hERG gene was transferred by lipofection; B: cell into which hERG gene was transferred with retrovirus; C: cell strain into which hERG gene was transferred with retrovirus; D: cell strain into which hERG gene was transferred with retrovirus and then cultured for one year continuously; E: cell strain into which hERG gene was transferred with lentivirus.)

Fig. 18 shows the hERG inhibitory activities of known compounds at various concentrations.

Fig. 19 shows changes in membrane potential caused by KCl, E4031 and Dofetilide which are hERG inhibitors.

BEST MODE FOR CARRYING OUT THE INVENTION

Hereinbelow, embodiments of the present invention will be described. The following embodiments are provided only for the purpose of illustration of the present invention. It is not intended to limit the present invention to the following embodiments. The present invention can be practiced in various other embodiments without departing from

the spirit of the invention.

In the present invention, it is possible to prepare a hERG gene-containing virus vector using a retrovirus or lentivirus vector plasmid and to allow cells to express hERG channels at high levels using the resultant virus vector. In the present invention, it is also possible to identify substances that inhibit hERG currents by using the hERG channel-expressing cell or cell population obtained by the present invention in measuring methods with a fully automated high throughput patch clamp system or a dye. Besides, the hERG channel-expressing cell or hERG channel-expressing cell population of the present invention is capable of expressing hERG channels stably for a long period of time.

In the present invention, the "patch clamp technique" or "patch clamping" refers to a technique to detect ionic flows passing through ion channels present on cell membranes with high sensitivity ("New Patch Clamp Experiment Technique", Yasunobu Okada Ed., Yoshioka Shoten). In the present invention, the term "conventional patch clamp technique" or "conventional patch clamping" refers to the whole cell patch clamp technique in which a highly skilled researcher presses glass microelectrodes 0.5-3 μm in diameter against a cell under microscopic observation to create a high resistant state and then destroys the relevant patch to thereby record currents passing through the ion channels present on the cell membrane surface.

In the present invention, the "patch clamp technique (or patch clamping) with a fully automated high throughput patch clamp system" refers to the perforated whole cell patch clamp technique where: cells are set in a measuring apparatus in a state of suspension in PBS or the like; perforated holes are formed on cell membrane surfaces with amphotericin B or the like; and ionic flows passing through ion channels present on cell surfaces are detected as currents.

In the present invention, the "fully automated high throughput patch clamp system" refers to an apparatus which sucks cells in suspension into a small hole in each well utilizing dropping by gravity and negative pressure, and to thereby make the recording of currents possible. Specific examples of fully automated high throughput patch clamp systems include IonWorks HT™ (Molecular Device) and PatchXpress™ 7000A (Axon Instruments).

In the present invention, hERG channel is one of the constituent proteins in the delayed rectifier potassium channel in cardiomyocytes and will be described later in detail.

In the present invention, hERG current refers to the flow of potassium ions passing through hERG channels present on cell membrane surfaces. The hERG channel is playing an important role in the heart to calm down electric excitement in cardiomyocytes. Drugs that inhibit the hERG current are compelled to withdraw from markets because such drugs

involve a risk of inducing serious ventricular arrhythmia. Therefore, it has become essential to develop drugs that have no or extremely small effect on the hERG channel in development of new drugs.

In the present invention, the "hERG current as determined by patch clamping with a fully automated high throughput patch clamp system" means the ionic current observed when the membrane potential of hERG channel-expressing cells is changed. More specifically, the hERG current is the ionic current that is detected when the membrane potential of the cell is changed from -80 mV to +20 mV for 1 sec and then to -50 mV for 1 sec. The peak value of the tail current observed when the membrane potential is restored to -50mV is taken as the amplitude of hERG current.

In the present invention, the "hERG channel-expressing cell" means a cell expressing hERG channels. Hereinbelow, a method of preparing a hERG channel-expressing cell or cell population will be described.

<hERG Channel>

In the present invention, the hERG channel to be expressed in cells contains a polypeptide containing an amino acid sequence identical or substantially identical with the amino acid sequence as shown in SEQ ID NO: 2 (GenBank Accession No. U04270) (hereinafter, sometimes referred to as the "polypeptide of the invention").

Hereinbelow, the polypeptide of the invention will be described in detail.

As the amino acid sequence substantially identical with the amino acid sequence as shown in SEQ ID NO: 2, an amino acid sequence which has about 90% or more, preferably about 95% or more, more preferably about 98% or more homology to the amino acid sequence as shown in SEQ ID NO: 2 and shows a polypeptide with hERG activity may be given.

In particular, in addition to the amino acid sequence above described, examples of the amino acid sequence substantially identical with the amino acid sequence as shown in SEQ ID NO: 2 include the amino acid sequence as shown in SEQ ID NO: 2 which has mutations such as deletion, substitution or addition in one or a plurality of (e.g., one or several) amino acids and shows a polypeptide with hERG activity.

Examples of the amino acid sequence as shown in SEQ ID NO: 2 which has mutations such as deletion, substitution or addition in one or a plurality of (e.g., one or several) amino acids include: (i) the amino acid sequence as shown in SEQ ID NO: 2 in which one to five (preferably one to three, more preferably one to two, still more preferably one) amino acids are deleted; (ii) the amino acid sequence as shown in SEQ ID NO: 2 to

which one to five (preferably one to three, more preferably one to two, still more preferably one) amino acids are added; (iii) the amino acid sequence as shown in SEQ ID NO: 2 into which one to five (preferably one to three, more preferably one to two, still more preferably one) amino acids are inserted; (iv) the amino acid sequence as shown in SEQ ID NO: 2 in which one to five (preferably one to three, more preferably one to two, still more preferably one) amino acids are substituted with other amino acids; and (v) an amino acid sequence which is a combination of (i) to (iv) above.

Further, a mutant polypeptide composed of the amino acid sequence having deletion, insertion, substitution or addition of one or a plurality of amino acids and retains the same biological activity of the initial polypeptide is also included in the scope of the present invention (Mark et al. (1984) Proc. Natl. Acad. Sci. USA 81: 5662-6; Zoller and Smith (1982) Nucleic Acids Res. 10: 6487-500; Wang et al. (1984) Science 224: 1431-3; Dalbadie-McFarland et al. (1982) Proc. Natl. Acad. Sci. USA 79: 6409-13).

Substitution of amino acids means a mutation in which one or more of amino acid residues in an amino acid sequence are replaced with other amino acids. In the modification of the amino acid sequence encoded by the hERG gene of the invention by such substitution, it is preferable to carry out a conservative substitution when it is necessary to retain the function of the protein. Conservative substitution means to change a sequence so that the changed sequence encodes an amino acid similar to the replaced amino acid in nature. Amino acids may be classified into non-polar amino acids (Ala, Ile, Leu, Met, Phe, Pro, Trp, Val), uncharged amino acids (Asn, Cys, Gln, Gly, Ser, Thr, Tyr), acidic amino acids (Asp, Glu), basic amino acids (Arg, His, Lys), neutral amino acids (Ala, Asn, Cys, Gln, Gly, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp, Tyr, Val), aliphatic amino acids (Ala, Gly), branched amino acids (Ile, Leu, Val), hydroxyl amino acids (Ser, Thr), amidic amino acids (Gln, Asn), sulfo-amino acids (Cys, Met), aromatic amino acids (His, Phe, Trp, Tyr), heterocyclic amino acids (His, Trp), imino acids (Pro, 4Hyp) and so on.

Therefore, it is preferable to carry out substitution between non-polar amino acids or between uncharged amino acids. Among all, substitutions between Ala, Val, Leu and Ile, between Ser and Thr, between Asp and Glu, between Asn and Gln, between Lys and Arg, and between Phe and Tyr are preferable for retaining the nature of the protein. The number and sites of amino acids to be mutated are not particularly limited.

Polynucleotides encoding the amino acid sequence as shown in SEQ ID NO: 2 having deletion, insertion, substitution or addition of one or a plurality of amino acids may be prepared according to methods such as site-specific mutagenesis described, for example, in "Molecular Cloning, A Laboratory Manual 2nd ed." (Cold Spring Harbor Press (1989)),

"Current Protocols in Molecular Biology" (John Wiley & Sons (1987-1997); especially in Section 8.1-8.5), Hashimoto-Goto et al. (1995) Gene 152: 271-5, Kunkel (1985) Proc. Natl. Acad. Sci. USA 82: 488-92, Kramer and Fritz (1987) Method. Enzymol. 154: 350-67, and Kunkel (1988) Method. Enzymol. 85: 2763-6.

Introduction of mutations into polynucleotides may be performed by known methods such as the Kunkel method or the Gapped duplex method using, for example, QuikChange™ Site-Directed Mutagenesis Kit (Stratagene), GeneTailor™ Site-Directed Mutagenesis System (Invitrogen), or TaKaRa Site-Directed Mutagenesis System (Mutan-K, Mutan-Super Express Km).

Amino acid residues composing the polypeptide of the invention may be either naturally occurring amino acid residues or modified amino acid residues. Specific examples of modification of amino acid residues include acylation, acetylation, amidation, arginylation, GPI anchor formation, cross-linking, γ-carboxylation, cyclization, formation of covalent bridges, glycosylation, oxidation, covalent bonding to lipid or fat derivatives, formation of disulfide bonds, selenoylation, demethylation, degradation treatment of proteins, covalent bonding to nucleotides or nucleotide derivatives, hydroxylation, formation of pyroglutamate, covalent bonding to flavin, prenylation, covalent bonding to heme moieties, covalent bonding to phosphatidylinositol, formylation, myristoylation, methylation, ubiquitination, iodination, racemization, ADP-ribosylation, sulfation and phosphorylation.

Further, the polypeptide of the invention encompasses fusion proteins where other peptide sequences have been added. Peptide sequences to be added to the polypeptide of the invention may be selected from sequences that make the discrimination of the protein easy or sequences that give stability when the protein is expressed by recombinant DNA technology, e.g., influenza hemagglutinin (HA), glutathione S transferase (GST), substance P, multiple histidine tag (6xHis, 10xHis, etc.), protein C fragment, maltose binding protein (MBP), immunoglobulin constant region fragment, α-tubulin fragment, β-galactosidase, B-tag, c-myc fragment, E-tag (epitope on monoclonal phage), FLAG (Hopp et al. (1988) Bio/Tehcnol. 6: 1204-10), lck tag, p18 HIV fragment, HSV-tag (human herpes simplex virus glycoprotein), SV40T antigen fragment, T7-tag (T7 gene10 protein), VSV-GP fragment (Vesicular stomatitis virus glycoprotein), etc.

As the polypeptide of the invention, the above-described polypeptide may be enumerated. A preferable example of the polypeptide of the invention is a polypeptide which contains the amino acid sequence as shown in SEQ ID NO: 2 or an amino acid sequence substantially identical with the amino acid sequence as shown in SEQ ID NO: 2 and has a hERG activity substantially identical in nature with the hERG activity possessed

by a polypeptide comoposed of the amino acid sequence as shown in SEQ ID NO: 2. The term "hERG activity" used herein means an activity of functioning as a potassium ion channel. The expression "activity substantially identical in nature" used herein means the relevant activity is identical in nature (e.g., physiochemically or pharmacologically).

<hERG Gene>

In the present invention, the "hERG gene" means a polynucleotide composed of a nucleotide sequence encoding a hERG channel. The hERG gene of the invention encompasses polynucleotides containing a nucleotide sequence identical or substantially identical with the nucleotide sequence as shown in SEQ ID NO: 1 (GenBank Accession No. U04270). A polynucleotide containing a nucleotide sequence substantially identical with the nucleotide sequence as shown in SEQ ID NO: 1 may be any polynucleotide as long as it has a nucleotide sequence encoding the above-described polypeptide of the invention. For example, in addition to polynucleotides encoding the amino acid sequence as shown in SEQ ID NO: 2, a polynucleotide encoding a mutant polypeptide composed of the amino acid sequence as shown in SEQ ID NO: 2 having deletion, insertion, substitution or addition of one or plurality of amino acids and has hERG activity may also be used in the present invention.

The term "polynucleotide" used herein refers to a polymer composed of a plurality of bases, such as deoxyribonucleic acid (DNA) or ribonucleic acid (RNA), or base pairs, and includes DNA, cDNA, genomic DNA, and chemically synthesized DNA and RNA. Polynucleotides optionally containing non-natural bases are also included in the term "polynucleotide". Specific examples of non-natural bases include 4-acetylcytidine, 5-(carboxyhydroxylmethyl)uridine, 2'-O-methylcytidine, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluridine, dihydrouridine, 2'-O-methylpseudouridine, β-D-galactosylqueosine, 2'-O-methylguanosine, inosine, N6-isopentenyladenosine, 1-methyladenosine, 1-methylpseudouridine, 1-methylguanosine, 1-methylinosine, 2,2-dimethylguanosine, 2-methyladenosine, 2-methylguanosine, 3-methylcytidine, 5-methylcytidine, N6-methyladenosine, 7-methylguanosine, 5-methylaminomethyluridine, 5-methoxyaminomethyl-2-thiouridine, β-D-mannosylqueosine, 5-methoxycarbonylmethyl-2-thiouridine, 5-methoxycarbonylmethyluridine, 5-methoxyuridine, 2-methylthio-N6-isopentenyladenosine, N-((9-β-D-ribofuranosyl-2-methyltiopurine-6-yl)carbamoyl)threonine, N-((9-β-D-ribofuranosylpurine-6-yl)N-methyl-carbamoyl)threonine, uridine-5-oxyacetic

acid-methyl ester, uridine-5-oxyacetic acid, wybutoxosine, pseudouridine, queosine, 2-thiocytidine, 5-methyl-2-thiouridine, 2-thiouridine, 4-thiouridine, 5-methyluridine, N-((9-β-D-ribofuranosylpurine-6-yl)carbamoyl)threonine, 2'-O-methyl-5-methyluridine, 2'-O-methyluridine, wybutosine and 3-(3-amino-3-carboxypropyl)uridine.

The hERG gene of the present invention encompasses genetic polymorphisms of the nucleotide sequence as shown in SEQ ID NO: 1. The genetic polymorphism may be easily known by using databases such as GenBank (http://www.ncbi.nlm.nih.gov). Genetic polymorphism includes single nucleotide polymorphism (SNP) and polymorphism caused by a varied number of nucleotide sequence repeats. Polymorphism caused by deletion or insertion of a plurality of nucleotides (e.g., two to several tens of nucleotides) is also included in genetic polymorphism. Besides, polymorphism where a sequence of two to several tens of nucleotides is repeated is also included in genetic polymorphism. Examples of these polymorphisms include VNTR (variable number of tandem repeat) (repeat unit composed of several to several tens of nucleotides) and micro-satellite polymorphism (repeat unit composed of about two to four nucleotides).

The hERG gene of the invention includes a nucleotide sequence encoding the amino acid sequence as shown in SEQ ID NO: 2. A nucleotide sequence encoding such an amino acid sequence encompasses, in addition to the nucleotide sequence as shown in SEQ ID NO: 1, nucleotide sequences which are different from SEQ ID NO: 1 because of the degeneracy of genetic codes. The nucleotide sequence as shown in SEQ ID NO: 1 from which non-coding regions are removed may also be used. When the polynucleotide of the invention is used for expressing a polypeptide by genetic engineering techniques, a nucleotide sequence with high expression efficiency may be selected and designed in view of the codon usage frequency in the cell to be used for expression (Grantham et al. (1981) Nucleic Acids Res. 9: 43-74).

Further, the hERG gene of the present invention encompasses a polynucleotide that hybridizes to the nucleotide sequence as shown in SEQ ID NO: 1 or a sequence complementary thereto under stringent conditions and encodes a polypeptide having hERG activity. Examples of such a polynucleotide include isoforms, alternative isoforms and allelic mutants; these are included in the hERG gene of the present invention. Such hERG genes may be obtained from human cDNA libraries or genomic libraries by a known hybridization method, such as colony hybridization, plaque hybridization or Southern blotting, using the polynucleotide composed of the nucleotide sequence as shown in SEQ ID NO: 1 or a fragment thereof as a probe. For methods for preparing cDNA libraries, see "Molecular Cloning, A Laboratory Manual 2nd Ed." (Cold Spring Harbor Press (1989)).

Alternatively, commercial cDNA libraries or genomic libraries may be used.

More specifically, in the preparation of a cDNA library, first, total RNA is prepared from a cell, organ or tissue that is expressing the hERG gene of the invention by a known method such as the guanidine ultracentrifugation method (Chirwin et al. (1979) Biochemistry 18: 5294-9) or the AGPC method (Chomczynski and Sacchi (1987) Anal. Biochem. 162: 156-9). Then, mRNA is purified therefrom by using mRNA Purification Kit (Pharmacia) or the like. Alternatively, a kit such as Quick Prep mRNA Purification Kit (Pharmacia) may be used to prepare mRNA directly from cells, organs or tissues. Subsequently, cDNA is synthesized from the resultant mRNA with a reverse transcriptase. A cDNA synthesis kit such as AMV Reverse Transcriptase First-Strand cDNA Synthesis Kit (Seikagaku Corporation) may also be used. Alternatively, cDNA may be synthesized and amplified by 5'-RACE method utilizing PCR (Frohman et al. (1988) Proc. Natl. Acad. Sci. USA 85: 8998-9002; Belyavsky et al. (1989) Nucleic Acids Res. 17: 2919-32). It is also possible to employ a known technique such as oligo-capping method (Maruyama and Sugano (1994) Gene 138: 171-4; Suzuki (1997) Gene 200: 149-56) in order to prepare a cDNA library with a high full-length cDNA ratio. The cDNA obtained as described above may be incorporated into an appropriate vector.

In the hybridization conditions used in the present invention, stringent conditions may be, for example, (2xSSC, 0.1%SDS, 50°C), (2xSSC, 0.1%SDS, 42°C) or (1xSSC, 0.1%SDS, 37°C); more stringent conditions may be, for example, (2xSSC, 0.1%SDS, 65°C), (0.5xSSC, 0.1%SDS, 42°C) or (0.2xSSC, 0.1%SDS, 65°C). More specifically, hybridization using Rapid-hyb buffer (Amersham Life Science) may be performed as described below, for example. Pre-hybridization is performed at 68°C for more than 30 min; then, a probe is added to the hybridization solution, which is retained at 68°C for more than 1 hr to allow hybrid formation; then, washing is carried out in 2xSSC, 0.1%SDS at room temperature for 20 min three times, in 1xSSC, 0.1%SDS at 37°C for 20 min three times, and finally in 1xSSC, 0.1%SDS at 50°C for 20 min two times. Alternatively, for example, pre-hybridization is performed in Expresshyb Hybridization Solution (CLONTECH) at 55°C for more than 30 min; a labeled probe is added to the solution, which is incubated at 37-55°C for more than 1 hr; then, washing is carried out in 2xSSC, 0.1%SDS at room temperature for 20 min three times and in 1xSSC, 0.1%SDS at 37°C for 20 min once. It is possible to make the hybridization conditions more stringent, for example, by raising the temperature of pre-hybridization, hybridization or second washing. For example, it is possible to set the temperature of pre-hybridization and hybridization at 60°C, or at 68°C for more stringent conditions. Those skilled in the art can appropriately select the salt

concentration and temperature of the buffer, as well as the concentration and length of the probe, reaction time, etc. to thereby set conditions for obtaining polynucleotides encoding the hERG gene of the invention.

For detailed procedures of hybridization, see "Molecular Cloning, A Laboratory Manual 2nd ed." (Cold Spring Harbor Press (1989); especially Section 9.47-9.58), "Current Protocols in Molecular Biology" (John Wiley & Sons (1987-1997); especially Section 6.3-6.4), "DNA Cloning 1: Core Techniques, A Practical Approach 2nd ed." (Oxford University (1995); especially, see Section 2.10 for conditions), and so forth. Examples of polynucleotides which hybridize to the nucleotide sequence as shown in SEQ ID NO: 1 or the sequence complementary thereto include polynucleotides containing a nucleotide sequence having 50% or more, preferably 70% or more, more preferably 80% or more, still more preferably 90% or more (e.g., 95% or more, or 99% or more) identity to the nucleotide sequence as shown in SEQ ID NO: 1. Such identity can be determined with BLAST algorithm (Altschul (1990) Proc. Natl. Acad. Sci. USA 87: 2264-8; Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90: 5873-7). Among programs based on this algorithm, there are programs for determining identity in sequences. BLASTX for amino acid sequence and BLASTN (Altschul et al. (1990) J. Mol. Biol. 215: 403-10) for nucleotide sequences have been developed and are available to the sequences of the present invention. For specific analyzing methods, see, for example, http://www.ncbi.nlm.nih.gov.

Genes whose structure and function are similar to those of hERG, such as isoforms or allelic mutants of hERG, (such genes are included in the hERG gene of the invention) may be obtained from human cDNA library or genomic library by using primers designed based on the nucleotide sequence as shown in SEQ ID NO: 1 and the gene amplification technique (PCR) (Current Protocols in Molecular Biology, John Wiley & Sons (1987) Section 6.1-6.4).

The polynucleotide of the invention encompasses polynucleotides encoding the amino acid sequence as shown in SEQ ID NO: 2 having deletion, insertion, substitution or addition of one or a plurality of amino acids, or sequences complementary to the sequences of these polynucleotides. These polynucleotides of the present invention may be prepared according to the site-specific mutagenesis method or the like described in "Molecular Cloning, A Laboratory Manual 2nd ed." (Cold Spring Harbor Press (1989)), "Current Protocols in Molecular Biology" (John Wiley & Sons (1987-1997); especially Section8.1-8.5), Hashimoto-Goto et al. (1995) Gene 152: 271-5, Kunkel (1985) Proc. Natl. Acad. Sci. USA 82: 488-92, Kramer and Fritz (1987) Method. Enzymol. 154: 350-67, Kunkel (1988) Method. Enzymol. 85: 2763-6, etc. The above-described commercial kits may be used for mutagenesis.

Confirmation of the nucleotide sequence of the polynucleotide of the invention may be performed by sequencing using conventional methods. For example, the dideoxynucleotide chain termination method (Sanger et al. (1977) Proc. Natl. Acad. Sci. USA 74: 5463) may be used. Alternatively, the sequence may be analyzed with an appropriate DNA sequencer.

<Virus Vector Plasmids>

According to the present invention, virus vector plasmids containing the hERG gene of the invention (hereinafter, sometimes referred to as the "virus vector plasmid of the invention") are provided. The term "virus vector plasmid" refers to a plasmid which was engineered by using a virus-derived nucleotide sequence so that it is capable of integrating any nucleotide sequence into any cell. The virus vector plasmid of the invention is useful in retaining the hERG gene of the invention within host cells and allowing the expression of the hERG channel encoded by the hERG gene.

As viruses which will be the basis for virus vector plasmids, oncoretrovirus-derived viruses such as Moloney murine leukemia virus (MoMLV) and lentivirus-derived viruses such as human immunodeficiency virus (HIV) may be enumerated.

In the present invention, retrovirus refers to any virus belonging to the genus Oncovirus in the subfamily Oncovirinae in the family Retroviridae, and lentivirus refers to any virus belonging to the genus Lentivirus in the subfamily Lentivirinae in the family Retroviridae.

It has been already shown that use of retrovirus vectors or lentivirus vectors efficiently enables stable transfer of genes into chromosomes of cells and their expression (Kay, M.A. et al. Nature Med. vol.7 33-40 (2001)). For the virus vector plasmid of the invention, various virus vector plasmids may be used. Specific examples include retrovirus vector plasmids such as pZIPneo (Cepko, C.L. et al. (1984) Cell. 37: 1053-1062), pBabePuro (Morgenstern, J.P. and Land, H. Nucleic Acids Res. vol.18 3587-3596), pCLXSN (IMGENEX, catalog #10041P), ViraPort retroviral gene expression system (Stratagene, catalog #217563), pDON-AI (Takara, catalog #3650) and lentivirus vector plasmids such as pLenti6/V5-GW/lacZ (Invitrogen, Carlsbad, CA, catalog #K4955-10). Further, virus vector plasmids prepared from viruses other than retrovirus and lentivirus may also be used. For example, vector plasmids prepared from adenovirus, adeno-associated virus, Sinbis virus, Sendai virus, togavirus, paramyxovirus, poxvirus, poliovirus, herpesvirus and vaccinia virus may be used.

Among retrovirus vectors, use of VSV-G pseudotyped retrovirus vectors is

preferable. The term "pseudotyped" refers to a phenomenon in which the genome of one virus is budding surrounded by the envelope protein of other virus (Zavada, J., J. Gen. Virol. vol.15 183-191 (1972)). Vesicular stomatitis virus (VSV) is a virus belonging to the family Rhabdoviridae and having a negative single-stranded RNA genome. It is believed that the receptor of its envelope protein (G protein) on the cell side is an anionic lipid such as phosphatidylserine (Schlegel, R. et al. Cell vol.32 639-646 (1983); Mastromarino, P. et al. J. Gen. Virol. vol.68 2359-2369 (1987)). It is reported that VSV-G pseudotyped retrovirus vector has an extremely broad host range compared to conventionally used amphotropic retrovirus vectors (Emi, N. et al., Proc. Natl. Acad. Sci. USA vol.65 1202-1207 (1991); Arai, T. et al. Virol. vol. 260 109-115 (1999)) and that its gene transfer ability can be improved by ultracentrifugation (Burns, J.C. et al. Proc. Natl. Acad. Sci. USA vol.90 8033-8037 (1993)). Therefore, by preparing a pseudotyped retrovirus having this VSV-G gene product as an envelope protein, it becomes possible to transfer the hERG gene into various cells more efficiently than achieved by retroviruses having their innate envelope protein.

The nature of these VSV-G pseudotyped vectors is the same in lentivirus vectors, and a large number of lentivirus vectors reported are pseudotyped vectors of this kind (Kay, M.A. et al. Nature Med. vol.7 33-40 (2001)).

In a preferred embodiment of virus vector plasmids, a virus vector plasmid is linked to downstream region of regulatory sequences so that it comes to enable the expression of the hERG gene of the invention in a host cell into which the virus vector plasmid has been introduced. The "regulatory sequences" are promoter and terminator, and optionally contain trans-activator, transcription factor, poly-A signal that stabilizes transcript, splicing and polyadenylation signals, and the like. These regulatory sequences contain all the components necessary for the expression of the polynucleotide linked thereto.

The virus vector of the invention may contain selectable markers. Examples of selectable markers include drug resistance genes (neomycin resistance gene, hygromycin resistance gene, puromycin resistance gene, etc.) and fluorescent proteins (GFP, EGFP, etc.). Further, it is possible to integrate a signal peptide that is necessary for directing the intracellularly expressed polypeptide onto cell membranes into a virus vector plasmid so that the signal peptide is added to the polypeptide. Further, addition of linker and insertion of initiation codon (ATG) and termination codon (TAA, TAG or TGA) may be performed, if necessary.

When a mammalian cell or other animal cell is used as a host, adenovirus late promoter (Kaufman et al. (1989) Mol. Cell. Biol. 9: 946), CAG promoter (Niwa et al. (1991) Gene 108: 193-200), CMV immediate early promoter (Seed and Aruffo (1987) Proc. Natl.

Acad. Sci. USA 84: 3365-9), EF1α promoter (Mizushima et al. (1990) Nucleic Acids Res. 18: 5322; Kim et al. (1990) Gene 91: 217-23), HSV TK promoter, SRα promoter (Takebe et al. (1988) Mol. Cell. Biol. 8: 466), SV40 promoter (Mulligan et al. (1979) Nature 277: 108), SV40 early promoter (Genetic Engineering Vol.3, Williamson ed., Academic Press (1982) pp.83-141), SV40 late promoter (Gheysen and Fiers (1982) J. Mol. Appl. Genet. 1: 385-94), RSV (Rous sarcoma virus)-LTR promoter (Cullen (1987) Methods Enzymol. 152: 684-704), MMLV-LTR promoter, CMV enhancer, SV40 enhancer, cPPT (central polypurine tract) sequence, globin intron, etc. may be used.

Insertion of the hERG gene into virus vector plasmids may be performed by ligase reaction. At this time, restriction enzyme sites may also be used (Current Protocols in Molecular Biology, John Wiley & Sons (1987) Section 11.4-11.11; Molecular Cloning, A Laboratory Manual 2nd ed., Cold Spring Harbor Press (1989) Section 5.61-5.63).

<Preparation of Virus Vectors>

In the present invention, the term "virus vector" means a virus containing a virus vector plasmid. For the preparation of a virus vector, a virus vector plasmid is introduced into a packaging cell. As a packaging cell, 293-EBNA cells (Invitrogen, catalog #R620-07) or the like may be used. A virus vector plasmid may be introduced into a packaging cell by various methods such as the adenovirus method, electroporation (Cytotechnology 3: 133 (1990)), the cationic liposome method (cationic liposome DOTAP (Boehringer Mannheim), etc.), the method using a positively charged polymer, the electrostatic type liposome method, the internal type liposome method, particle gun bombardment, the liposome method, lipofection (Proc. Natl. Acad. Sci. USA 84: 7413 (1987) (e.g., lipofectamine 2000 (Invitrogen), Fugene 6 (Roche Diagnostics), etc.)), the calcium phosphate method (JP 2-227075 A), receptor-mediated gene transfer, the retrovirus method, the DEAE dextran method, the virus-liposome method (Experimental Medicine additional volume "Basic Technology for Gene Therapy", Yodo-sha (1997); Experimental Medicine additional volume "Analytical Experiments on Gene Transfer and Expression", Yodo-sha (1997); J. Clin. Invest. 93: 1458-64 (1994); Am. J. Physiol. 271: R1212-20 (1996); Molecular Medicine 30: 1440-8 (1993); Experimental Medicine 12: 1822-6 (1994); Protein, Nucleic Acid and Enzyme, 42: 1806-13 (1997); Circulation 92 (Suppl. II): 479-82 (1995)) and direct transfer of naked-DNA.

Briefly, a virus vector may be obtained by culturing a packaging cell in an appropriate medium, transfecting a virus vector plasmid into the cell by the above-mentioned method, then culturing the cell for a specific period of time, and recovering the resultant

culture. After the transfection, if necessary, the medium may be exchanged 2 to 24 hours, preferably 6 to 12 hours thereafter. After the medium exchange, the cell is cultured for another 12 to 72 hours. Then, a virus vector can be obtained by recovering the culture. If necessary, the recovered culture may be centrifuged or filtered with, for example, a 0.45 μm filter (Millipore, MILLEX-HV, catalog #SLHV025LS).

<Concentration of Virus Vectors>

Although the virus vector of the invention may be used as it is, it is preferable to concentrate the virus vector. A concentrated virus vector may be obtained by ultracentrifuging the virus vector obtained by the above-described procedures. Ultracentrifugation is performed at least at 35,000 g (g represents gravitational acceleration) or more, preferably 55,000 g or more, at least for 100 min or more, preferably 120 min or more. Ultracentrifugation can be achieved, for example, with an ultracentrifuge XL-90 (Beckman) and an ultracentrifuge rotor SW28 (Beckman) at 19,500 rpm for 100 min.

<hERG Gene Transfer>

In the present invention, the hERG gene transfer into cells may be performed by using the virus vector of the invention as it is. However, use of a concentrated virus vector is preferable.

As a host cell in the hERG channel-expressing cell or hERG channel-expressing cell population of the invention, a mammal-derived eukaryotic cell may be used. Preferably, CHO cells (especially, DHFR gene deficient dhfr$^-$ CHO (Proc. Natl. Acad. Sci. USA 77: 4216-20, 1980) and CHO K-1 (Proc. Natl. Acad. Sci. USA 60: 1275, 1968) are preferable), COS cells, Hela cells, C127 cells, 3T3 cells, BHK cells, HEK293 cells, Bowes melanoma cells and the like may be used. It is also possible to use a heart-derived cell line or an isolated cardiomyocyte or sinoatrial node cell as a host cell in the hERG channel-expressing cell or hERG channel-expressing cell population of the invention. The hERG channel-expressing cell or cell population of the invention also includes those cells which are capable of regulating transcription and thereby regulating expression under specific conditions (e.g., under drug stimulation, electric stimulation, thermal stimulation, photo stimulation, or the like).

Gene transfer can be achieved by culturing a host cell, adding a virus vector to the culture, and culturing further. Preferably, a concentrated virus vector is used. If necessary, polybrene (Sigma H9268, also known as hexadimethrine bromide) may be added to the virus vector to be added to the culture. Twenty-four hours after the addition of the virus, it is

preferable to exchange the medium. It is possible to make the expression level per cell highest by culturing the cell for about 72 hours after the medium exchange.

<hERG Channel-Expressing Cell and hERG Channel-Expressing Cell Population>

By the procedures described so far, the hERG channel-expressing cell or hERG channel-expressing cell population of the invention is provided. Culture is performed by a known method suitable for the selected cell. For example, medium such as DMEM, MEM, RPMI1640, IMDM or F12 may be used. If necessary, serum such as fetal calf serum (FCS), amino acid, glucose, penicillin or streptomycin, and the like may be added thereto. The cell may be cultured at about pH 6-8 at 30-40°C for about 15-200 hours. During the course of culture, medium may be exchanged, and aeration and agitation may be carried out, if necessary.

In the cell population of hERG gene-transferred cells obtained by the method of the invention (hereinafter, sometimes referred to as the "hERG channel-expressing cell population of the invention"), a large number of channel-expressing cells (hereinafter, referred to as the "hERG channel-expressing cell of the invention") are present. Inter alia, the hERG channel-expressing cell population of the invention contains a plenty of hERG channel expressing cells of which the hERG current as determined by patch clamping with a fully automated high throughput patch clamp system is 0.6 nA or more. The ratio of such cells in the total number of hERG gene-transferred cells is at least 40% or more, preferably 50% or more, more preferably 60% or more, especially preferably 70% or more, and most preferably 80% or more. With respect to the hERG gene-transferred cells, as long as the contents of gene transfer operations are the same, the total number of cells into which the gene was transferred in the same experiment system may be taken as the parameter, or cells into which the gene was transferred in different experiment systems (e.g., experiments conducted on different days) may be summed up and the total may be taken as the parameter. The average amplitude of hERG currents in the hERG channel-expressing cell population is 0.3 nA or more, preferably 0.6 nA or more, more preferably 0.8 nA or more, still more preferably 1.0 nA or more.

The hERG current of the hERG channel-expressing cell or hERG channel-expressing cell population as determined by patch clamping with a fully automated high throughput patch clamp system may be determined by the patch clamp technique described later. The ratio of hERG channel-expressing cells of which the hERG current as determined by patch clamping with a fully automated high throughput patch clamp system is 0.6 nA or more can be obtained by selecting a plurality of cells at random, measuring the

hERG current of each of these cells, and then calculating the ratio of those cells of which the hERG current is 0.6 nA or more.

The hERG channel-expressing cell or hERG channel-expressing cell population of the invention also encompasses those cells or cell strains obtained by the cloning described later. Further, the hERG channel-expressing cell or hERG channel-expressing cell population of the invention also encompasses those cells or cell populations that are obtained by transferring the hERG gene again into the cell strain obtained by the cloning.

<Cloning of hERG Channel-Expressing Cell>

Although the hERG channel-expressing cell or hERG channel-expressing cell population of the invention may be used as it is, the cell or the cell population may be subjected to cloning in order to avoid bias in nature during culture and to enable stable evaluation of drugs. Cell cloning may be performed according to conventional methods (such as the limiting dilution culture method or cell sorting by flow cytometry). It is possible to select from the cloned cell strains hERG channel-expressing cell strains which are more suitable for measurement of expression levels and functional analysis of hERG channel by the patch clamp technique.

hERG channel expression levels in hERG channel-expressing cells may be determined by immunohistological analysis methods using anti-hERG channel antibody. The antibodies may be prepared according to conventional methods. Alternatively, a commercial antibody (such as prepared by Alomene Labs) may be used. Examples of immunohistological analysis methods include enzyme immunoassay (EIA), radioimmunoassay (RIA), ELISA, Western blotting, flow cytometry, and immunohistochemical staining.

By this cloning, cells of which the hERG current as determined by patch clamping with a fully automated high throughput patch clamp system is at least 0.4 nA or more, preferably 0.6 nA or more, more preferably 0.8 nA or more, still more preferably 1.0 nA or more, especially preferably 1.2 nA or more, are provided more easily.

<Method of Measurement of hERG Currents>

The present invention provides a method of measuring hERG currents by using the hERG channel-expressing cell or hERG channel-expressing cell population of the invention. More specifically, the present invention provides a method of measuring hERG currents using the hERG channel-expressing cell or hERG channel-expressing cell population of the invention by the patch clamp technique, preferably with a fully automated high throughput

patch clamp system,

A hERG channel-expressing cell or hERG channel-expressing cell population may be obtained by the above-described method of preparing the hERG channel-expressing cell of the invention. For the hERG channel expression level of the hERG channel expressing cell used in the method of measurement of hERG currents of the invention, the channel current as determined by patch clamping with a fully automated high throughput patch clamp system is preferably at least 0.4 nA or more, preferably 0.6 nA or more, more preferably 0.8 nA or more, still more preferably 1.0 nA or more, especially preferably 1.2 nA or more. Such a hERG channel-expressing cell or hERG channel-expressing cell population is also included in the scope of the present invention. It should be noted here that the higher the expression level is, the higher the channel current as determined by patch clamp technique becomes.

For practicing the method of measuring hERG currents of the invention, the hERG channel-expressing cell or cell population of the invention is cultured for a specific period of time by the appropriate method as described above and suspended in a buffer suitable for measurement. As the buffer, any buffer which does not affect hERG currents may be used, e.g., phosphate buffer or Tris-HCl buffer at pH 6-8. Preferably, phosphate buffered saline (pH 7.4) is used.

Subsequently, hERG currents may be recorded by the patch clamp technique, preferably with a fully automated high throughput patch clamp system. hERG currents may be induced by giving various holding potentials and depolarizing pulses to cells. These conditions may be easily set by those skilled in the art (Zhou, Z. et al., Biophysical Journal, 74, 230-241 (1998)). For example, hERG currents may be induced by changing the holding potential from -80 mV to +20 mV for 1 sec and then applying a depolarizing pulse to -50 mV for 1 sec. As the amplitude of hERG current, the peak value of the tail current observed when the potential is restored to -50 mV may be used.

<Method of Measuring hERG Current Inhibitory Activities Using the hERG Channel-Expressing Cell of the Invention>

It is known that compounds with hERG current inhibitory activity have arrhythmogenesis effect accompanied by QT interval prolongation effect. Such compounds may induce serious adverse effects such as ventricular tachycardia or sudden death. Therefore, in the development of highly safe pharmaceuticals, it is essential to confirm that the test substance (target of development) does not affect hERG currents. The method of measuring hERG current inhibitory activities using the hERG channel-expressing cell of the

invention facilitates the selection of test compounds that do not affect hERG currents. Therefore, the method of measuring inhibitory activities of the invention is useful in developing pharmaceuticals such as therapeutics and prophylactics for various diseases.

The present invention provides a method of measuring hERG current inhibitory activities by using a hERG channel-expressing cell or a hERG channel-expressing cell population. Specifically, the present invention provides a method of measuring hERG current inhibitory activities by contacting a test compound with the hERG channel-expressing cell or cell population of the invention. In the measurement of hERG current inhibitory activities of the present invention, it is possible to measure hERG currents of the hERG channel-expressing cell or cell population of the invention before and after contacting a test compound with the cell or cell population, and compare the results. For example, hERG current inhibitory activities may be determined by using as an indicator the ratio of the amplitude of hERG current after contacting a test compound to the amplitude of hERG current before contacting the test compound.

The present invention further provides a method of screening for compounds, or salts thereof, that alter or do not alter hERG currents, by using a hERG channel-expressing cell or cell population. Specifically, the present invention provides a method of screening for compounds, or salts thereof, that alter or do not alter hERG currents, by comparing the case of contacting a test compound with the hERG channel-expressing cell or cell population of the invention and the case of not contacting the test compound with the cell or cell population. In the screening method of the present invention, it is possible to measure hERG currents of the hERG channel-expressing cell or cell population of the invention in the case of contacting and in the case of non-contacting, and to compare the results. For example, when the hERG current in the case of contacting the test compound is smaller than the hERG current in the case of non-contacting the test compound, the test compound can be regarded as a hERG channel current inhibitory compound.

As the hERG channel-expressing cell or cell population, the hERG channel-expressing cell of the invention or the hERG channel-expressing cell population of the invention may be used. Alternatively, such a cell or cell population may be obtained by the method of the invention for preparing a hERG channel-expressing cell or cell population described above. In the method of measuring hERG current inhibitory activities of the invention, for the hERG channel expression level of the hERG channel expressing cell or cell population of the invention, the channel current as determined by patch clamping with a fully automated high throughput patch clamp system is at least 0.4 nA or more, preferably 0.6 nA or more, more preferably 0.8 nA or more, still more preferably 1.0 nA or more,

especially preferably 1.2 nA or more. It should be noted here that the higher the expression level is, the higher the channel current as determined by the patch clamp technique becomes; thus, construction of a more sensitive measuring system becomes possible.

In order to practice the method of the invention described above, the hERG channel-expressing cell or cell population of the invention is cultured for a specific period of time by the appropriate method as described above and suspended in a buffer suitable for measurement. As the buffer, any buffer which does not affect hERG currents may be used, e.g., phosphate buffer or Tris-HCl buffer at pH 6-8. Preferably, phosphate buffered saline (pH 7.4) is used.

First, hERG currents may be recorded by the patch clamp technique, preferably with a fully automated high throughput patch clamp system. hERG currents may be induced by giving various holding potentials and depolarizing pulses to cells. These conditions may be easily set by those skilled in the art. For example, hERG currents may be induced by changing the holding potential from -80 mV to +20 mV for 1 sec and then applying a depolarizing pulse to -50 mV for 1 sec. As the amplitude of hERG current, the peak value of the tail current observed when the potential is restored may be used.

Subsequently, a test compound is allowed to co-exist with the hERG channel-expressing cell. At this time, the cell without the test compound and the cell with compounds which are known to inhibit hERG currents may also be prepared as controls. Specific examples of compounds that inhibit hERG currents include astemizole (Talialatel et al. (1998) Mol. Pharmacol. 54: 113-21), E-4031 (Zhou et al. Biophys. J. (1998) 74: 230-41), risperidone (Kongsamut et al. Eur. J. Pharmacol. (2002) 450: 37-41), verapamil (Zhang et al. (1999) Circ. Res. 84: 989-98) and quinidine (Jiesheng et al. J. Pharmacol. Exp. Ther. (2001) 299: 290-6). The reaction is performed, for example, at 15-37°C, preferably at 20-30 °C, for 10 sec to 60 min, preferably for 3 min to 10 min.

Then, hERG currents may be recorded by the patch clamp technique, preferably with a fully automated high throughput patch clamp system. hERG currents may be induced under the same conditions as used before the co-existence with the test compound. As the amplitude of hERG current, the peak value of the tail current observed when the potential is restored may be used.

For example, the amplitude of the hERG current before the contact with the test compound is taken as 100% and 0 nA is taken as 0%. Then, inhibition ratio is calculated from the amplitude of the hERG current after the contact with the test compound, followed by determination of the hERG current inhibitory activity of the test compound. Further, it is also possible to calculate the inhibitory activity value inherent in the test compound by

varying the dose of the test compound. When the concentration of the test compound inducing 50% inhibition of hERG currents is at least 0.3 μM or more, preferably 1.0 μM or more, more preferably 3.0 μM or more, especially preferably 10 μM or more, most preferably 30 μM or more, the test compound can be judged as not affecting hERG currents or not having inhibitory activity.

Examples of test compounds include peptides, proteins, non-peptidic compounds, synthetic compounds, fermentation products, cell extracts, plant extracts and animal tissue extract. These compounds may be either novel compounds or known compounds.

<Method of Measuring Changes in Membrane Potential on hERG Channel-Expressing Cell of the Invention with FLIPR Membrane Potential Assay Kit>

The present invention provides a method of measuring changes in membrane potential on the hERG channel-expressing cell using FLIPR Membrane Potential Assay Kit (Molecular Devices).

Specifically, changes in membrane potential may be measured by performing the following operations in a manner as described below. The hERG channel-expressing cell of the invention is cultured for a specific period of time by the appropriate method as described above and suspended in a buffer suitable for measurement. As the buffer, any buffer which does not affect hERG currents may be used, e.g., phosphate buffer or Tris-HCl buffer at pH 6-8. Preferably, phosphate buffered saline (pH 7.4) is used. It is preferred that the cell suspension be prepared to give a concentration of 0.2×10^5 cells/ml to 1.0×10^6 cells/ml. Subsequently, the cell suspension is plated on plates (such as Biocoat Poly-D-Lysine 384-Well Black/Clear Plate; BECKTON DICKINSON) and cultured further. Cells may be plated at 500 cells/well to 25000 cells/well. Preferably, cells are cultured for about two days after the plating. Subsequently, Component A contained in FLIPR Membrane Potential Assay Kit (Molecular Devices) is dissolved in a measurement buffer (130 mM NaCl, 5 mM KCl, 1 mM $MgCl_2$, 1 mM $CaCl_2$, 24 mM Glucose, 10 mM HEPES (final pH: approx. 7.25)), and a 25 μl aliquot of this solution is added to each well. About one hour after the addition of Component A, changes in membrane potential may be measured with FLIPR (Molecular Devices) or FDSS6000 (Hamamatsu Photonics). As the measuring program, the appropriate condition may be set by those skilled in the art. For example, measurement may be performed 10 times before the addition of a test compound and 50 times after the addition, both at 6 second intervals. Measurement may be performed at room temperature. hERG inhibitory activity may be calculated from the change in fluorescence intensity caused by the addition of the test compound. As positive controls,

E4031, Dofetilide and the like may be used.

In the specification and drawings of the present application, the abbreviations used for nucleotides, amino acids and so forth are those recommended by the IUPAC-IUB Commission on Biochemical Nomenclature or those conventionally used in the art. Examples of such abbreviations are given below. Amino acids that may have optical isomers are intended to represent their L-isomer unless otherwise specified.

DNA: Deoxyribonucleic acid
cDNA: Complementary deoxyribonucleic acid
A: Adenine
T: Thymine
G: Guanine
C: Cytosine
RNA: Ribonucleic acid
mRNA: Messenger ribonucleic acid
Gly or G: Glycine
Ala or A: Alanine
Val or V: Valine
Leu or L: Leucine
Ile or I: Isoleucine
Ser or S: Serine
Thr or T: Threonine
Cys or C: Cysteine
Met or M: Methionine
Glu or E: Glutamic acid
Asp or D: Aspartic acid
Lys or K: Lysine
Arg or R: Arginine
His or H: Histidine
Phe or F: Phenylalanine
Tyr or Y: Tyrosine
Trp or W: Tryptophan
Pro or P: Proline
Asn or N: Asparagine
Gln or Q: Glutamine

The sequence ID numbers in the sequence listing of the specification of the present patent application represent the following sequences.

[SEQ ID NO: 1] This shows the nucleotide sequence represented by GenBank Accession No. U04270.

[SEQ ID NO: 2] This shows the amino acid sequence represented by GenBank Accession No. U04270.

[SEQ ID NO: 3] This shows the nucleotide sequence of a primer for cloning hERG gene.

[SEQ ID NO: 4] This shows the nucleotide sequence of a primer for cloning hERG gene.

[SEQ ID NO: 5] This shows the nucleotide sequence of a primer for cloning hERG gene.

[SEQ ID NO: 6] This shows the nucleotide sequence of a primer for cloning hERG gene.

[SEQ ID NO: 7] This shows the nucleotide sequence of a primer for cloning hERG gene.

[SEQ ID NO: 8] This shows the nucleotide sequence of a primer for cloning hERG gene.

[SEQ ID NO: 9] This shows a nucleotide sequence to insert a multicloning site.

[SEQ ID NO: 10] This shows a nucleotide sequence to insert a multicloning site.

[SEQ ID NO: 11] This shows a nucleotide sequence to insert a central polypurine tract.

[SEQ ID NO: 12] This shows a nucleotide sequence to insert a central polypurine tract.

[SEQ ID NO: 13] This shows the nucleotide sequence of pBabe Puro.

EXAMPLES

Hereinbelow, the present invention will be described in more detail with reference to the following Examples. However, the present invention is not restricted to these Examples.

[EXAMPLE 1] Preparation of hERG Gene

A hERG gene was isolated as described below by using the nucleotide sequence as shown in SEQ ID NO: 1 as a basis. In this sequence, 4070 bps are shown in which the region encoding a hERG channel (excluding the stop codon) is said nucleotides 184 to 3660 (3477 bps, 1159 amino acid residues) (GenBank Accession No. U04270). In order to isolate the gene by PCR (polymerase chain reaction), oligo DNA primers as shown in SEQ ID NO: 3 to 8 were prepared by Japan Bio Service (Asaka City, Saitama) upon request of the inventors.

cDNA was prepared by using human brain polyA+ RNA (Clontech, Palo Alto, CA, catalog #6516-1) as a template with Superscript First-Strand Synthesis System (Invitrogen/Gibco, MD). Subsequently, by using the resultant cDNA as a template and

oligo DNAs consisting of SEQ ID NO: 3 and 4, SEQ ID NO: 5 and 6 and SEQ ID NO: 7 and 8 as primers, PCR reactions were performed with Expand High Fidelity PCR System (Roche Diagnostics, Mannheim, Germany) by repeating 30 cycles of 95°C for 30 sec, 61°C for 30 sec and 68°C for 1 min. The nucleotide sequences of the primers are as described below.

Primer: AATTGGTACCATGGGCTCAGGATGCCGGTGC (SEQ ID NO: 3)
Primer: GCTTGTACTCAGGCAGCACGT (SEQ ID NO: 4)
Primer: CCACCAGTGACCGTGAGATCA (SEQ ID NO: 5)
Primer: TTGCAGTGCTGCAGCAGTGAG (SEQ ID NO: 6)
Primer: ATGCTAGCATCTTCGGCAACG (SEQ ID NO: 7)
Primer: AATTAAGCTTTTTCGAGTTCCTCTCCCCTTC (SEQ ID NO: 8)

As a result, DNA fragments of approx. 1.2 kb, 1.2 kb and 1.6 kb, respectively, were obtained.

These DNA fragments were inserted into pT7Blue (Novagen, Darmstadt, Germany, catalog #69967-3) and sequenced by using ABI prism DNA sequencing kit (Perkin-Elmer Applied Biosystems, Foster City, CA) for confirmation. As a result, a 1179 bps sequence obtained with the primer pair consisting of SEQ ID NO: 3 and 4 was identical with the nucleotides 173 to 1351 in SEQ ID NO: 1. On the other hand, a 1168 bps sequence obtained with the primer pair consisting of SEQ ID NO: 5 and 6 had two mutations (A1875G and T2149C). It is clear that these mutations do not influence the amino acids translated from the nucleotide sequences of the relevant sites (Leu and Thr). A 1642 bps sequence obtained with the primer pair consisting of SEQ ID NO: 7 and 8 also had two mutations (C2420T and A3367G). Since a plurality of clones obtained this time had the same mutations, it was judged that this sequence was correct as a hERG gene in the sample used this time (human brain polyA+ RNA (Clontech, Palo Alto, CA, catalog #6516-1)).

pBluescript (Stratagene, La Jolla, CA) was digested with restriction enzymes KpnI and XhoI. On the other hand, the DNA fragment obtained with the primer pair consisting of SEQ ID NO: 3 and 4 was digested with restriction enzymes KpnI and BstEII, and the DNA fragment obtained with the primer pair consisting of SEQ ID NO: 5 and 6 was digested with restriction enzymes BstEII and XhoI. Subsequently, the resultant DNA fragments were inserted into the KpnI/XhoI-digested pBluescript by ligase reaction (TaKaRa, Cat.6022) to thereby prepare pBS-1&14&15&18.

pBluescript was digested with restriction enzymes HindIII and XhoI. On the other hand, the DNA fragment obtained with the primer pair consisting of SEQ ID NO: 7 and 8 was digested with restriction enzymes HindIII and SacI. The resultant DNA

fragment was inserted into the HindIII/XhoI-digested pBluescript by ligase reaction to thereby prepare pBS-6&4.

Further, pREP7 (Invitrogen, Carlsbad, CA) was digested with KpnI and HindIII. On the other hand, pBS-1&14&15&18 was digested with KpnI and XhoI, and pBS-6&4 was digested with XhoI and HindIII. The resultant DNA fragments were inserted into KpnI/HindIII-digested pREP7 by ligase reaction to thereby obtain pREP7HERG containing a hERG gene.

[EXAMPLE 2] Preparation of Retrovirus Vector Plasmids

pBabe Puro (Morgenstern, J.P. and Land, H., Nucleic Acids Res. vol.18 3587-3596) (SEQ ID NO: 13) was digested with restriction enzymes SalI and ClaI to remove SV40 promoter-puro(r) and then blunt-ended with Klenow fragment (Takara, Otsu, Japan). Into this site, IRES-puro(r) that had been cut out from pIRESpuro (Clontech, Palo Alto, CA, catalog #6031-1) with restriction enzymes NsiI and XbaI and then blunt-ended with T4 polymerase was inserted to thereby obtain pBabeXIP (Fig. 1).

pBabe Puro (Morgenstern, J.P. and Land, H., Nucleic Acids Res. vol.18 3587-3596) (SEQ ID NO: 13) was digested with SalI and ClaI to remove SV40 promoter-puro(r) and then blunt-ended with Klenow fragment. Into this site, IRES-hyg(r) that had been cut out from pIREShyg (Clontech, Palo Alto, CA, catalog #6061-1) with restriction enzymes NsiI and XbaI and then blunt-ended with T4 polymerase was inserted to thereby obtain pBabeXIH (Fig. 2).

pBabeXIP was digested with restriction enzymes SspI and BamHI to remove 5'-LTR-packaging signal. Into this site, 5'LTR-CMV promoter-packaging signal that had been cut out from pCLXSN (IMGENEX San Diego, CA, catalog #10041P) with restriction enzymes SspI and BamHI was inserted to thereby obtain pBabeCLXIP (Fig. 3).

pBabeXIH was digested with SspI and BamHI to remove 5'-LTR-packaging signal. Into this site, 5'LTR-CMV promoter-packaging signal that had been cut out from pCLXSN (IMGENEX San Diego, CA, catalog #10041P) with SspI and BamHI was inserted to thereby obtain pBabeCLXIH (Fig. 4).

pBabeCLXIH was digested with restriction enzyme BglII to remove IRES-hyg(r) and then blunt-ended with Klenow fragment. Into this site, IRES-EGFP that had been cut out from pIRES2-EGFP (Clontech, Palo Alto, CA, catalog #6029-1) with restriction enzyme HincII was inserted to thereby obtain pBabeCLXI2G (Fig. 5).

pBabeCLXIH was digested with BglII to remove IRES-hyg(r) and then blunt-ended with Klenow fragment. Into this site, IRES-neo(r) that had been cut out from

pIRES2-neo2 (Clontech, Palo Alto, CA, catalog #6938-1) with NsiI and XbaI and then blunt-ended with T4 polymerase was inserted to thereby obtain pBabeCLXaIN (Fig. 6).

[EXAMPLE 3] Preparation of Retrovirus Vector Plasmids for hERG Gene Transfer

pBabeCLXaIN obtained in Example 2 was digested with restriction enzyme HpaI. Into this site, a hERG gene that had been cut out from pREP7HERG (obtained in Example 1) with KpnI and HindIII and then blunt-ended with T4 polymerase was inserted to thereby obtain pBabeCL(hERG)aIN (Fig. 7).

pBabeCLXIH obtained in Example 2 was digested with HpaI. Into this site, a hERG gene that had been cut out from pREP7HERG (obtained in Example 1) with KpnI and HindIII and then blunt-ended with T4 polymerase was inserted to thereby obtain pBabeCL(hERG)IH (Fig. 8).

pBabeCLXIP obtained in Example 2 was digested with HpaI. Into this site, a hERG gene that had been cut out from pREP7HERG (obtained in Example 1) with KpnI and HindIII and then blunt-ended with T4 polymerase was inserted to thereby obtain pBabeCL(hERG)IP (Fig. 9).

pBabeCLXI2G obtained in Example 2 was digested with HpaI. Into this site, a hERG gene that had been cut out from pREP7HERG (obtained in Example 1) with KpnI and HindIII and then blunt-ended with T4 polymerase was inserted to thereby obtain pBabeCL(hERG)I2G (Fig. 10).

pBabeCLXIH obtained in Example 2 was digested with BglII to remove IRES-hyg(r) and then blunt-ended with Klenow fragment. Into this site, a hERG gene that had been cut out from pREP7HERG (obtained in Example 1) with KpnI and HindIII and then blunt-ended with T4 polymerase was inserted to thereby obtain pBabeCL(hERG) (Fig. 11).

[EXAMPLE 4] Preparation of Lentivirus Vector Plasmids

In order to insert a multicloning site, oligo DNAs consisting of SEQ ID NO: 9 and 10 were prepared by Japan Bio Service (Asaka City, Saitama) upon request of the inventors. The nucleotide sequences of the oligo DNAs were as follows.

oligo DNA:

GATCCCCCGGGCTGCAGGAATTCGATATCGTTAACGTCGACCTCGAGGGTAC (SEQ ID NO: 9)

oligo DNA:

CCTCGAGGTCGACGTTAACGATATCGAATTCCTGCAGCCCGGGG (SEQ ID NO:

10)

The oligo DNAs of SEQ ID NO: 9 and 10 were annealed by thermally denaturing at 98°C for 5 min and then slowly returning to room temperature.

pLenti6/V5-GW/lacZ (Invitrogen, Carlsbad, CA, catalog #K4955-10) was digested with restriction enzymes BamHI and KpnI to remove lacZ-V5 epitope-SV40 early promoter-EM7 promoter-blasticidin(r). Into this site, the above-described oligo DNA was inserted to thereby obtain pLenti6/MCS (Fig. 12).

In order to introduce central polypurine tract (cPPT) for enhancing gene transfer ability, oligo DNA primers as shown in SEQ ID NO: 11 and 12 were prepared by Japan Bio Service (Asaka City, Saitama) upon request of the inventors with reference to a previously reported method (Zennou, V.Z. et al., Cell vol. 101 173-185 (2000)).

Primer: GTCGTCATCGATACAAATGGCAGTATTCATCC (SEQ ID NO: 11)

Primer: GTCGTCAAGCTTCCAAACTGGATCTCTGCTGTCC (SEQ ID NO: 12)

By using the oligo DNAs consisting of SEQ ID NO: 11 and 12 as primers and plasmid pLP1 (ViraPower Lentiviral Gateway Expression kit, Invitrogen; K4960-00) as a template, PCR was performed with Expand High Fidelity PCR System (Roche Diagnostics, Mannheim, Germany). The thermal conditions were 30 cycles of 95°C for 30 sec, 61°C for 30 sec and 68°C for 1 min. As a result, a DNA fragment of approx. 0.2 kb was obtained. This DNA fragment was inserted into pT7Blue (Novagen, Darmstadt, Germany, catalog #69967-3) to thereby obtain cPPT-pT7Blue. The nucleotide sequence of the DNA fragment was confirmed with ABI prism DNA sequencing kit (Perkin-Elmer Applied Biosystems, Foster City, CA) to be identical with the already reported sequence of cPPT (Zennou, V.Z. et al., Cell vol.101 173-185 (2000)).

pBluescript (Stratagene) was digested with restriction enzymes ClaI and BamHI. Into this site, ClaI/HindIII-digested cPPT-pT7Blue containing cPPT and BamHI/HindIII-digested pLenti6/MCS containing CMV promoter was inserted to thereby obtain cPPT-CMV-pBS.

pLenti6/MCS was digested with ClaI and BamHI to remove CMV promoter. Into this site, ClaI/BamHI-digested cPPT-CMV-pBS containing cPPT-CMV promoter was inserted to thereby obtain pLenti6/cPPT-MCS, which was then digested with KpnI and blunt-ended with T4 polymerase. Into this site, IRES-EGFP fragment that had been cut out from pIRES2-EGFP (Clontech, catalog #6029-1) with HincII was inserted to thereby obtain pLenti6/cPPT-XI2G (Fig. 13).

[EXAMPLE 5] Preparation of Lentivirus Vector Plasmid for hERG Gene Transfer

pLenti6/cPPT-XI2G obtained in Example 4 was digested with EcoRI and SalI. Into this site, a hERG gene that had been cut out from pBabeCL(hERG)I2G (obtained in Example 3) with EcoRI and SalI and then blunt-ended with T4 polymerase was inserted to thereby obtain pLenti6/cPPT-(hERG)I2G (Fig. 14).

[EXAMPLE 6] Preparation of Vector Plasmid

pREP7HERG obtained in Example 1 was digested with KpnI and HindIII to cut out the hERG gene, which was inserted into KpnI/HindIII-digested pZeoSV2 (Invitrogen) to thereby obtain pZeohERG.

pZeohERG was introduced into a dam$^-$ *E. coli* strain SCS110, which was then mass-cultured and subjected to plasmid preparation. SV40 promoter-hERG gene (ClaI/fill-in-HindIII) obtained from the resultant plasmid was introduced into a DNA fragment (NurI/HindIII digested product) that had been obtained from pcDNA3.1 Neo by removing CMV promoter to thereby prepare pSV hERG-Neo. The mass culture of the expression vector-introduced *E. coli* was conducted by conventional methods. The purification of the vector was conducted by using EndoFree Plasmid Kit (Qiagen).

[EXAMPLE 7] Preparation of Retrovirus Vector for hERG Gene Transfer

293-EBNA cells (Invitrogen, catalog #R620-07) ($2x10^6$ cells) were cultured in 10 ml of DMEM (Sigma catalog #D5796)-10% fetal bovine serum (FCS)-penicillin/streptomycin (PS) (hereinafter, referred to as "EBNA culture medium") in 10 cm collagen-coated dishes (IWAKI, Tokyo, catalog #4020-010). Next day, 3.3 μg each of pV-gp (obtained from pVPack-GP (Stratagene, catalog #217566) by digesting with NsiI and XbaI to remove IRES-hisD, blunt-ending with T4 polymerase and then self-ligating), pVPack-VSV-G (Stratagene, catalog #217567) and pBabeCL(hERG)I2G obtained in Example 3 were transfected into the cells by using a lipofection reagent TransIT (Panvera, Madison, WI, catalog #MIR2300). Six to twelve hours after the transfection, EBNA culture medium was exchanged and culture was continued at 37°C.

Two days after the transfection, the culture medium was recovered and centrifuged at 1,200 g for 10 min. The resultant supernatant was filtered through a 0.45 μm filter (Millipore, MILLEX-HV, catalog #SLHV025LS) to thereby obtain a non-concentrated retrovirus vector, which was used in subsequent experiments.

[EXAMPLE 8] Preparation of Lentivirus Vector for hERG Gene Transfer

293-EBNA cells (Invitrogen, catalog #R620-07) ($4x10^6$ cells) were cultured in 10 ml of DMEM (Sigma, catalog #D5796)-10% fetal bovine serum (FCS)-penicillin/streptomycin (PS) (hereinafter, referred to as "EBNA culture medium") in 10 cm collagen-coated dishes (IWAKI, Tokyo, catalog #4020-010). Next day, 2.5 μg each of pLP1, pLP2, pLP/VSVG (all from Invitrogen, catalog #K4970-10) and the lentivirus vector plasmid for human hERG gene transfer obtained in Example 5 were transfected into the cells by using a lipofection reagent TransIT (Panvera, Madison, WI, catalog #MIR2300). Six to twelve hours after the transfection, EBNA culture medium was exchanged and culture was continued at 37°C.

Two days after the transfection, the culture medium was recovered and centrifuged at 1,200 g for 10 min. The resultant supernatant was filtered through a 0.45 μm filter (Millipore, MILLEX-HV, catalog #SLHV025LS) to thereby obtain a non-concentrated lentivirus vector, which was used in subsequent experiments.

[EXAMPLE 9] Concentration of the Retrovirus Vector

The virus vector prepared in Example 7 was concentrated as described below. Ultracentrifuge tubes (50 Ultra-Clear Tubes, Beckman, Palo Alto, CA, catalog #344058) were sterilized with 70% ethanol and rinsed with distilled water. Into each tube, approx. 35 ml of the non-concentrated virus vector was transferred. The tubes were placed in SW28 ultracentrifuge rotor (Beckman) and centrifuged at 19,500 rpm for 100 min using ultracentrifuge equipment XL-90 (Beckman). After the centrifugation, the supernatant was discarded and each tube was left in ice. After one hour, a concentrated virus vector solution was obtained in a form of approx. 100 μl of culture remaining on the tube wall. If necessary, concentrated virus vector solutions were collected and subjected to ultracentrifugation again to thereby prepare a re-concentrated virus vector solution.

[EXAMPLE 10] Concentration of the Lentivirus Vector

The virus vector prepared in Example 8 was concentrated as described below. Ultracentrifuge tubes (50 Ultra-Clear Tubes, Beckman, Palo Alto, CA, catalog #344058) were sterilized with 70% ethanol and rinsed with distilled water. Into each tube, approx. 35 ml of the non-concentrated virus vector was transferred. The tubes were placed in SW28 ultracentrifuge rotor (Beckman) and centrifuged at 19,500 rpm for 100 min using ultracentrifuge equipment XL-90 (Beckman). After the centrifugation, the supernatant was discarded and each tube was left in ice. After one hour, a concentrated virus vector solution was obtained in a form of approx. 100 μl of culture remaining on the tube wall. If

necessary, concentrated virus vector solutions were collected and subjected to ultracentrifugation again to thereby prepare a re-concentrated virus vector solution.

[EXAMPLE 11] Preparation of hERG-Expressing Cells with Retrovirus Vector for hERG Gene Transfer (1)

hERG gene transfer into cell with the virus vector prepared in Example 7 was performed as described below.

Briefly, Chinese Hamster Ovary (CHO)-K1 cells (Cell Bank, RIKEN Gene Bank) (3×10^3 cells) were cultured in 100 μl of DMEM/F12 (Invitrogen Corp., catalog #11320-033)-10% fetal bovine serum (FCS)-penicillin/streptomycin (PS) (hereinafter, referred to as "CHO culture medium") in 96 well plates (Becton-Dickinson, Franklin Lakes, NJ catalog #35-3075). The next day, 100 μl of the virus vector prepared in Example 7 was added to the CHO cells together with polybrene (final concentration: 8 μg/ml) (Sigma H9268; also known as hexadimethrine bromide) diluted with the culture medium. The next day, the culture medium containing the virus vector was exchanged with 200 μl of the CHO culture medium. The culture was continued for another three days. The resultant hERG gene-transferred cells were subjected to the following experiments to know rough natures of them as a cell population. If necessary, the cells were subjected to the cell cloning as described later in Example 18, before use in the following experiments.

[EXAMPLE 12] Preparation of hERG-Expressing Cells with Lentivirus Vector for hERG Gene Transfer (2)

hERG gene transfer into cell with the virus vector prepared in Example 8 was performed as described below.

Briefly, Chinese Hamster Ovary (CHO)-K1 cells (Cell Bank, RIKEN Gene Bank) (3×10^3 cells) were cultured in 100 μl of DMEM/F12 (Invitrogen Corp., catalog #11320-033)-10% fetal bovine serum (FCS)-penicillin/streptomycin (PS) (hereinafter, referred to as "CHO culture medium") in 96 well plates (Becton-Dickinson, Franklin Lakes, NJ, catalog #35-3075). The next day, 100 μl of the virus vector prepared in Example 8 was added to the CHO cells together with polybrene (final concentration: 8 μg/ml) (Sigma H9268; also known as hexadimethrine bromide) diluted with the culture medium. The next day, the culture medium containing the virus vector was exchanged with 200 μl of the CHO culture medium. The culture was continued for another three days. The resultant hERG gene-transferred cells were subjected to the following experiments to know rough natures of them as a cell population. If necessary, the cells were subjected to the cell cloning as

described later in Examples 17 and 18, before use in the following experiments.

[EXAMPLE 13] Preparation of hERG-Expressing Cells with Retrovirus Vector for hERG Gene Transfer (2)

hERG gene transfer into cell with the centrifuge-concentrated virus vector from Example 9 was performed as described below.

Briefly, Chinese Hamster Ovary (CHO)-K1 cells (Cell Bank, RIKEN Gene Bank) (3×10^3 cells) were cultured in 100 μl of DMEM/F12 (Invitrogen Corp., catalog #11320-033)-10% fetal bovine serum (FCS)-penicillin/streptomycin (PS) (hereinafter, referred to as "CHO culture medium") in 96 well plates (Becton-Dickinson, Franklin Lakes, NJ, catalog #35-3075). The next day, 100 μl of the centrifuge-concentrated virus vector from Example 9 was added to the CHO cells together with polybrene (final concentration: 8 μg/ml) (Sigma H9268; also known as hexadimethrine bromide) diluted with the culture medium. The next day, the culture medium containing the virus vector was exchanged with 200 μl of the CHO culture medium. The culture was continued for another three days. The resultant hERG gene-transferred cells were subjected to the following experiments to know rough natures of them as a cell population. If necessary, the cells were subjected to the cell cloning as described later in Example 18, before use in the following experiments.

[EXAMPLE 14] Preparation of hERG-Expressing Cells with Retrovirus Vector for hERG Gene Transfer (3)

The cell cloning described in Example 18 was performed to select a cell strain in which an appropriate hERG current could be recorded. hERG gene was transferred into the resultant cell strain with the centrifuge-concentrated virus vector from Example 9 as described below.

A hERG-expressing cell strain (3×10^3 cells) obtained in Example 13 was cultured in 100 μl of DMEM/F12 (Invitrogen Corp., catalog #11320-033)-10% fetal bovine serum (FCS)-penicillin/streptomycin (PS) (hereinafter, referred to as "CHO culture medium") in 96 well plates (Becton-Dickinson, Franklin Lakes, NJ, catalog #35-3075). The next day, 100 μl of the centrifuge-concentrated virus vector from Example 9 was added to the CHO cells to give a final concentration of 8 μg/ml, together with polybrene (final concentration: 8 μg/ml) (Sigma H9268; also known as hexadimethrine bromide) diluted with the culture medium. The next day, the culture medium containing the virus vector was exchanged with 200 μl of the CHO culture medium. The culture was continued for another three days. The resultant hERG gene-transferred cells were subjected to the following experiments to know

rough natures of them as a cell population. If necessary, the cells were subjected to the cell cloning as described later in Example 18, before use in the following experiments.

[EXAMPLE 15] Preparation of hERG-Expressing Cells with Lentivirus Vector for hERG Gene Transfer (2)

hERG gene transfer into cell with the virus vector prepared in Example 10 was performed as described below.

Briefly, Chinese Hamster Ovary (CHO)-K1 cells (Cell Bank, RIKEN Gene Bank) (3×10^3 cells) were cultured in 100 μl of DMEM/F12 (Invitrogen Corp., catalog #11320-033)-10% fetal bovine serum (FCS)-penicillin/streptomycin (PS) (hereinafter, referred to as "CHO culture medium") in 96 well plates (Becton-Dickinson, Franklin Lakes, NJ, catalog #35-3075). The next day, 100 μl of the centrifuge-concentrated virus vector from Example 10 was added to the CHO cells together with polybrene (final concentration: 8 μg/ml) (Sigma H9268; also known as hexadimethrine bromide) diluted with the culture medium. The next day, the culture medium containing the virus vector was exchanged with 200 μl of the CHO culture medium. The culture was continued for another three days. The resultant hERG gene-transferred cells were subjected to the following experiments to know rough natures of them as a cell population. If necessary, the cells were subjected to the cell cloning as described later in Examples 17 and 18, before use in the following experiments.

[EXAMPLE 16] Preparation of hERG-Expressing Cells by Lipofection with hERG Gene Transfer Vector

hERG gene transfer vector was introduced into CHO-K1 cells (Cell Bank, Riken Gene Bank) as described below in accordance with Effectene Transfection Reagent Handbook.

To a 2-day culture of the CHO-K1 cells in culture dishes 6 cm in diameter were added approx. 1 μg of hERG expression vector (SV-hERG-neo) dissolved in TE solution and 8 μl of enhancer which were mixed to give a final volume of 150 μl and agitated for approx. 1 sec, and left stationary for 2-5 min at room temperature. Subsequently, 25 μl of Effectene Transfection Reagent was added thereto. The mixture was agitated for approx. 10 sec and left stationary for 5-10 min at room temperature. Then, 1 ml of the medium was added thereto. The cells were washed with PBS(-), transferred into a culture dish containing 4 ml of medium, and cultured in an incubator at 37°C under 5% CO_2. The next day, cells were taken off from the culture dish with trypsin and suspended in a medium containing G418 that

is 500 μg in potency. After several days of culture, cells were subjected to the cell cloning as described in Example 18 before use in the following experiments.

[EXAMPLE 17] Isolation and Concentration of hERG High Expressing Cells by FACS with GFP Expression as an Indicator

From the hERG-transferred cells prepared in Example 12 or 15, those cells that express hERG still higher were isolated and concentrated by using FACSAria (Becton Dickinson) with GFP expression as an indicator. Briefly, cells prepared in 10 cm dishes were taken off with trypsin, and GFP high expressing cells alone were isolated according to the protocol of FACSAria and analyzed. The results of analysis revealed that GFP high expressing cells were concentrated. The resultant cells were subjected to the cell cloning as described in Example 18 before use in the following experiments.

[EXAMPLE 18] Cloning of hERG Channel-Expressing Cells

The cloning of cells was performed by the limiting dilution culture method. A cell suspension was prepared so that each well of 96-well culture plates contained 0.3 cells. A 200 μl aliquot of the cell suspension was dispensed into each well. About two weeks later, under microscopic observation, cells of those wells where a single cell population (colony) was observed in a single well were transferred into 24-well culture plates and cultured further. Thereafter, the scale of culture was expanded to F75 culture flask. From the resultant cells, hERG channel-expressing cell strains were selected by Western blotting to confirm protein expression and electrophysiological techniques to confirm functional expression of hERG channel (Examples 19 and 20).

[EXAMPLE 19] Detection of hERG Channel by Western Blotting

This experiment was conducted by using CHO-K1 cells, the cell strain into which hERG gene was transferred by lipofection (Example 16) and the cell strain into which hERG gene was transferred with retrovirus (Example 14). Individual cells cultured in 6-well plates were washed with ice-cooled PBS. Then, a lysis buffer (150 mmol/L NaCl, 50 mmol/L Tris-HCl (pH 7.5), 5 mmol/L EDTA, 0.5% Nonidet R P-40, 0.5% deoxycholic acid sodium) supplemented with Protease Inhibitor Cocktail (SIGMA-Aldrich Co.) was added thereto, and the cells were scraped off with a cell scraper. The resultant cells were collected in Eppendorf tubes and centrifuged at 4°C at 10,000 rpm (centrifuge: MRX-152, rotor: TMA-6; TOMY SEIKO) for 3 min. The resultant supernatants were recovered as samples. Protein concentrations in samples were determined with BCA Protein Assay Kit (Pierce

Biotechnology Inc., Rockford, IL, USA).

Electrophoresis and transfer of proteins were examined with NOVEX (Invitrogen) apparatuses. Briefly, appropriate amounts of NuPAGE LDS Sample Buffer (Invitrogen) and NuPAGE Sample Reducing Agent (Invitrogen) were added to the recovered sample and heated at 95°C for 3 min. The resultant sample was applied to NuPAGE 3-8% Tris-Acetate Gel (Invitrogen) and electrophoresed at 120V for about one hour using NuPAGE Tris-Acetate Running Buffer (Invitrogen). The resultant gel was mounted in Xcell Surelock™ (Invitrogen) together with Immun-Blot PVDF Membrane (Bio-Rad Laboratories, Inc.) and transferred at 30V for about one hour by using NuPAGE Transfer Buffer (Invitrogen).

Anti-HERG (Alomone Labs) was used as a primary antibody, and anti-rabbit IgG HRP-linked antibody (Cell Signaling Technology, Inc.) was used as a secondary antibody. After primary antibody reaction and secondary antibody reaction, the PVDF Membrane was washed with 0.1% Tween20/PBS. Detection of bound antibody was performed with ECL detection kit (Amersham Biosciences Corp.).

As a result, a band of a molecular weight of approx. 150 kD corresponding to the hERG protein was not detected in normal CHO-K1 cells (Fig. 15, lane 1). A weak band of the hERG protein was detected in cell strain M3 which was established by hERG gene transfer by lipofection (Fig. 15, lane 2). In contrast, a large amount of the hERG protein was detected clearly in the cell strain into which hERG gene was transferred with retrovirus (Fig. 15, lane 3).

[EXAMPLE 20] Measurement of hERG Current with Fully Automated High Throughput Patch Clamp System and Comparison of Current Distribution

This experiment was conducted by using the cell strain into which hERG gene was transferred by lipofection (Example 16) and the cell (Example 13) and the cell strain (Example 14) into each of which hERG gene was transferred with retrovirus. hERG channel-expressing cells were cultured in F75 culture flasks. Then, cells were taken off from the F75 culture flasks with EDTA-containing PBS(-) solution and suspended in PBS solution to give an appropriate concentration (1.0-1.5 x 10^6 cells/ml). The cell suspension was transferred into a cell reserver in IonWorks HT™ system. Procedures for measuring hERG currents were as follows. First, PBS was dispensed into each well of measuring plates (PatchPlate™, Molecular Devices Corp.). Then, the cell suspension was dispensed into each well and left until cells formed a seal in a hole at the center of each well. After seal formation, an amphotericin B-containing solution (KCl 140mM, $MgCl_2$ 1mM, EGTA

1mM, HEPES 20mM, pH 7.25-7.3) was perfused to allow formation of a perforated patch. After perforated patch formation, potential changes were given to cells by the voltage clamp method through stimulation electrodes to induce hERG currents, followed by recording the hERG currents.

Briefly, hERG currents were induced by changing the potential from -80 mV to +20 mV for 1 sec and then to -50 mV for 1 sec. The peak value of the tail current observed when the potential was restored to -50 mV was taken as the amplitude of hERG current. The distributions of hERG currents recorded in the cell strain into which hERG gene was transferred by lipofection and the cell strains into which hERG gene was transferred with retrovirus are shown in Fig. 16 and Table 1.

The hERG current distribution in the cell which was established by hERG gene transfer with retrovirus (Example 13) (Panel B of Table 1 and Fig. 16) was larger than that in the cell strain which was established by hERG gene transfer by lipofection (Example 16) (Panel A of Table 1 and Fig. 16), and the hERG current distribution in the cell strain (Example 14) was definitely still larger (Panel C of Table 1 and Fig. 16).

Table 1

A

Amplitude (nA)	0-0.2	0.2-0.4	0.4-0.6	0.6-0.8	0.8-1.0	1.0-1.2	1.2-1.4	1.4-1.6	1.6-1.8	1.8-2.0	2.0-2.2	2.2-2.4	> 2.4	SUM
number	240	21	1	1	0	1	0	0	0	0	0	0	0	264
ratio (%)	90.9	8.0	0.4	0.4	0.0	0.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0

B

Amplitude (nA)	0-0.2	0.2-0.4	0.4-0.6	0.6-0.8	0.8-1.0	1.0-1.2	1.2-1.4	1.4-1.6	1.6-1.8	1.8-2.0	2.0-2.2	2.2-2.4	> 2.4	SUM
number	12	61	66	48	28	15	16	9	6	5	1	0	1	268
ratio (%)	4.5	22.8	24.6	17.9	10.4	5.6	6.0	3.4	2.2	1.9	0.4	0.0	0.4	100.0

C

Amplitude (nA)	0-0.2	0.2-0.4	0.4-0.6	0.6-0.8	0.8-1.0	1.0-1.2	1.2-1.4	1.4-1.6	1.6-1.8	1.8-2.0	2.0-2.2	2.2-2.4	> 2.4	SUM
number	17	19	27	34	53	48	45	26	25	16	7	6	5	328
ratio (%)	5.2	5.8	8.2	10.4	16.2	14.6	13.7	7.9	7.6	4.9	2.1	1.8	1.5	100.0

In Table 1, A, B and C represent hERG current distributions in the cell strain into which hERG gene was transferred by lipofection, the cell into which hERG gene was transferred with retrovirus, and the cell strain into which hERG gene was transferred with retrovirus, respectively.

Further, in order to evaluate the hERG current inhibitory activities of compounds more stably, cut-off values were set, followed by analysis of hERG currents in individual hERG-expressing cells. As for cut-off values, (1) the ratio of the peak value of the tail current to the value of current when depolarized to +20 mV that is less than 0.8; and (2) seal

resistance that is less than 30 MΩ were set. Data satisfying these conditions were analyzed.

The results of analysis with the cut-off values are shown in Fig. 17 and Table 2.

The hERG current distribution in the cell which was established by hERG gene transfer with retrovirus (Example 13) (Panel B of Table 2 and Fig. 17) was larger than that in the cell strain which was established by hERG gene transfer by lipofection (Example 16) (Panel A of Table 2 and Fig. 17), and the hERG current distribution in the cell strain (Example 14) (Panel C of Table 2 and Fig. 17) was definitely still larger. Further, the hERG current in the cell which had been cultured continuously for one year was stable (Panel D of Table 2 and Fig. 17). Besides, the hERG current distribution in the cell strain that was established by hERG gene transfer with lentivirus was also definitely as large as that seen in the cell strain established with retrovirus. This meant that hERG channels are expressed stably even after one year continuous cultivation (Panel E of Table 2 and Fig. 17).

Table 2

A

Amplitude(nA)	0-0.2	0.2-0.4	0.4-0.6	0.6-0.8	0.8-1.0	1.0-1.2	1.2-1.4	1.4-1.6	1.6-1.8	1.8-2.0	2.0-2.2	2.2-2.4	> 2.4	SUM
number	8	19	1	0	0	1	0	0	0	0	0	0	0	29
ratio (%)	27.6	65.5	3.4	0.0	0.0	3.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0

B

Amplitude (nA)	0-0.2	0.2-0.4	0.4-0.6	0.6-0.8	0.8-1.0	1.0-1.2	1.2-1.4	1.4-1.6	1.6-1.8	1.8-2.0	2.0-2.2	2.2-2.4	> 2.4	SUM
number	11	60	65	46	28	15	16	9	7	4	1	0	1	263
ratio (%)	4.2	22.8	24.7	17.5	10.6	5.7	6.1	3.4	2.7	1.5	0.4	0.0	0.4	100.0

C

Amplitude(nA)	0-0.2	0.2-0.4	0.4-0.6	0.6-0.8	0.8-1.0	1.0-1.2	1.2-1.4	1.4-1.6	1.6-1.8	1.8-2.0	2.0-2.2	2.2-2.4	> 2.4	SUM
number	1	14	38	62	59	39	33	20	18	8	5	2	3	302
ratio (%)	0.3	4.6	12.6	20.5	19.5	12.9	10.9	6.6	6.0	2.6	1.7	0.7	1.0	100.0

D

	0-0.2	0.2-0.4	0.4-0.6	0.6-0.8	0.8-1.0	1.0-1.2	1.2-1.4	1.4-1.6	1.6-1.8	1.8-2.0	2.0-2.2	2.2-2.4	> 2.4	SUM
number	2	32	55	81	66	37	18	20	17	4	3	3	5	343
ratio (%)	0.6	9.3	16.0	23.6	19.2	10.8	5.2	5.8	5.0	1.2	0.9	0.9	1.5	100.0

E

Amplitude(nA)	0-0.2	0.2-0.4	0.4-0.6	0.6-0.8	0.8-1.0	1.0-1.2	1.2-1.4	1.4-1.6	1.6-1.8	1.8-2.0	2.0-2.2	2.2-2.4	> 2.4	SUM
number	0	19	55	67	49	36	19	7	13	2	1	3	0	271
ratio (%)	0.0	7.0	20.3	24.7	18.1	13.3	7.0	2.6	4.8	0.7	0.4	1.1	0.0	100.0

In Table 2, A, B, C, D and E represent hERG current distributions in the cell strain into which hERG gene was transferred by lipofection, the cell into which hERG gene was transferred with retrovirus, the cell strain into which hERG gene was transferred with retrovirus, the cell strain into which hERG gene was transferred with retrovirus and then cultured for one year continuously, and the cell strain into which hERG gene was transferred

with lentivirus, respectively.

[EXAMPLE 21] Evaluation of the hERG Channel Inhibitory Activities of Test Compounds with Fully Automated High Throughput Patch Clamp System

This experiment was conducted by using the cell strain into which hERG gene was transferred by lipofection (Example 16) and the cell strain into which hERG gene was transferred with retrovirus (Example 14). hERG currents were measured in the same manner as described in Example 20. With respect to the inhibitory activities of test compounds or known compounds against hERG channels, inhibition ratios were calculated from the ratios of the peak value of the tail current after the addition of various concentrations of test compounds, taking the peak value of the tail current recorded before the addition of the relevant test compound as 100%. From the inhibition ratios of test compounds at individual concentrations, hERG current inhibitory activity values (IC_{50}) were calculated.

Each drug was evaluated at the following concentrations: 0.016, 0.048, 0.014, 0.041, 0.123, 0.37, 1.11 and 3.33 μM for astemizole, E-4031, risperidone and verapamil; and 0.048, 0.014, 0.041, 0.123, 0.37, 1.11, 3.33 and 10 μM for quinidine. The drugs were allowed to act for about 4 min.

The results revealed that, while most of the data points were missing in the cell strain into which hERG gene was transferred by lipofection, all the data could be obtained in the cell strain into which hERG gene was transferred with retrovirus. Also, the IC_{50} values of individual drugs (0.083, 0.044, 0.536, 0.720 and 0.385 μM) could be obtained in the latter cell strain (Fig. 18).

[EXAMPLE 22] Measurement of Changes in Membrane Potential with FLIPR Membrane Potential Assay Kit

This experiment was conducted on the cell strain into which hERG gene was transferred with retrovirus (Example 14) by using FLIPR Membrane Potential Assay Kit (Molecular Devices) and FDSS6000 (Hamamatsu Photonics). hERG channel-expressing cells were plated on Biocoat Poly-D-Lysine 384-Well Black/Clear Plate (BECKTON DICKINSON) two days before measurement. Briefly, a cell suspension was prepared to give a concentration of 1.2×10^5 cells/ml, and a 25 μl aliquot of this suspension was dispensed into each well. Component A contained in FLIPR Membrane Potential Assay Kit was dissolved in a measurement buffer (130 mM NaCl, 5 mM KCl, 1 mM $MgCl_2$, 1 mM $CaCl_2$, 24 mM Glucose, 10 mM HEPES (final pH: approx. 7.25)), and a 25 μl aliquot of this

solution was added to each well. About one hour after the addition of Component A, changes in membrane potential were measured with FDSS6000. The measuring program was as follows: 10 times before the addition of a test substance, 50 times after the addition and at 6 second intervals. Measurement was performed at room temperature. hERG inhibitory activity was calculated from the fluorescence intensity change for 5 min after the addition of the test substance. As positive controls, E4031 and Dofetilide were used.

The results are shown in Fig. 19. Changes in fluorescence intensity that mean the membrane potential was depolarized by the addition of KCl were observed. Similar changes in the membrane potential were also caused by E4031 and Dofetilide which are hERG inhibitors, and the changes depended on the concentration of these inhibitors.

[EXAMPLE 23] Recording of hERG Currents by Conventional Patch Clamp Technique

The recording of hERG currents by the conventional patch clamp technique was conducted by using the hERG-expressing cells of the present invention. The measurement of hERG currents was performed as described below with reference to Zhou, Z. et al., Biophysical Journal, 74, 230-241 (1998).

Cells were plated on polylysine-coated glass plates and cultured for 2 to 4 days. At measurement the resultant glass plates were transferred into a current measurement bath. hERG currents were observed by the voltage clamp method of the whole cell patch clamp technique. As solutions for recording of hERG currents, an extracellular perfusion solution (NaCl 137 mM, KCl 4 mM, $MgCl_2$ 1 mM, $CaCl_2$ 1.8 mM, glucose 10 mM, HEPES 10 mM, pH7.4) and an intraelectrode solution (KCl 130 mM, $MgCl_2$ 1 mM, Mg-ATP 5 mM, EGTA 5 mM, HEPES 10 mM, pH7.2) were used. For measuring hERG currents, a current amplifier (Axon Instruments) was used. For recording and analyzing hERG currents, pCLAMP software (Axon Instruments) was used. hERG currents were induced in cells by changing the potential from -80 mV to +20 mV for 5 sec and then to -50 mV for 4 sec, at 20 sec intervals. The peak value of the tail current observed when the potential was restored to -50 mV was used as the amplitude of hERG current.

INDUSTRIAL APPLICABILITY

According to the present invention, a method of establishing a cell with a remarkably high hERG channel expression level for use in predicting adverse effects based on hERG channel inhibition in research and development of drugs has been established. With this method, highly sensitive and high throughput evaluation has become possible.

Further, according to the present invention, hERG channel high expressing cells

can be obtained simultaneously and efficiently. With this advantage, by allowing a wide variety of cell species to express hERG gene at high levels and comparing influences of endogenous ion channels among those cell species, it has become possible to select the most suitable cell species for predicting adverse effects in research and development of drugs. Further, the hERG channel-expressing cell or hERG channel-expressing cell population of the present invention is capable of expressing hERG channels stably for a long period of time.

SEQUENCE LISTING FREE TEXT

SEQ ID NO: 3: primer
SEQ ID NO: 4: primer
SEQ ID NO: 5: primer
SEQ ID NO: 6: primer
SEQ ID NO: 7: primer
SEQ ID NO: 8: primer
SEQ ID NO: 9: oligo DNA
SEQ ID NO: 10: oligo DNA
SEQ ID NO: 11: primer
SEQ ID NO: 12: primer

The publications cited in the present specification are incorporated herein in their entirety.